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INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-020-956-109

Alignment Scores:
Pred. No.: 8,44e-287 Length: 1524
Score: 320.00 Matches: 320
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 28.4% Indels: 0
DB: 3 Gaps: 0

US-10-643-795a-123 (1-1127) x US-09-020-956-109 (1-1524)

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QY 766 LeuArgGInGlyLeuSerGlyGlyGlySerLeuAlaSerGlyGlyProGlyProGly 785
DB 10 CTGCGCCAGGCGCTGAGCGGAGCGGCGGCGAGCTCGCCAGCGGCGGCGGCGCTGAGC 69
QY 786 HisAlaSerLeuSerGlnArgLeuArgLeuTyrLeuAlaAspSerTrpAngInGlyAsp 805
DB 70 CATGCTCTACCTAGCCAGCGGCGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 129
QY 806 LeuValAlaLeuThrCysPheLeuLeuGlyValGlyCysArgLeuThrProGlyLeuTyr 825
DB 130 CTAGAGGCTCTACCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 189
QY 826 HisLeuGlyArgThrValLeuGlyCysIleAspPheMetValPheThrValArgLeuHis 845
DB 190 CACCTGGGCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 249
QY 846 IlePheThrValAsnIleGlnLeuGlyProGlyValLeuAlaSerIleMetCys 865
DB 250 ATCTTCACGCTCAACAAAGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 309
QY 866 AspValPhePhePheLeuPhePheLeuGlyValTyrLeuValAlaTyrGlyValAlaThr 885
DB 310 GACGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 369
QY 886 GlnGlyLeuLeuArgProArgAspSerAspPheProSerIleLeuArgArgValPheTyr 905
DB 370 GAGGGGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTCTCT 429
QY 906 ArgProTyrLeuGlnIlePheGlyGlnIleProGlnIleAspMetAspValAlaLeuMet 925
DB 430 CTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 489
QY 926 GlnHisSerAsnCysSerSerGlyProGlyPheTyrAlaIleProProGlyValAlaGln 945
DB 490 GAGCAAGCAAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 549
QY 946 GlyThrCysValSerGlnTyrAlaAsnTyrLeuValValLeuLeuValIlePheLeu 965
DB 550 GGCACCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 609
QY 966 LeuValAlaAsnIleLeuLeuValIleLeuLeuLeuIleAlaMetPheSerTyrThrPheGly 985
DB 610 CTCTGCGGCAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 669
QY 986 LysValGlnGlyAsnSerAspLeuTyrTyrPylValGlnArgTyrArgLeuIleArgGln 1005
DB 670 AAAGTACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 729
QY 1006 PheHisSerArgProAlaLeuAlaProPheIleValIleSerHisLeuArgLeu 1025
DB 730 TTCACCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 789
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QY 1026 LeuArgGlnLeuCysArgArgProArgSerProGlnProSerSerProAlaLeuGlnHis 1045
DB 790 CTGAGGCAATGTGTGAGGCGAGCCCGGAGCCCGGAGCGGCTCTCTCTCTCTCTCTCT 849
QY 1046 PheArgValTyrLeuSerLysGlnAlaGlnArgLysLeuLeuThrTyrGlnSerValHis 1065
DB 850 TTCCGGGTTTACCTTTCTTCAAGGAAGCCGAGCGGGAAGCTTCACTGCGGAATCGGTGCAT 909
QY 1066 LysGlnAsnPheLeuLeuValArgAlaArgAspLysArgGlnSerAspSerGlnArgLeu 1085
DB 910 AAGGAACCTTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 969
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RESULTS

US-10-643-795a-123 (1-1127) x US-09-020-956-109 (1-1524)
Sequence identity: 100%
Patent No. 6,262,215
US/09030607

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FC
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/030,607
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 109:

SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:

ORGANISM: Homo sapiens
US-09-030-607-109

Alignment Scores:

Pred. No.: 8,44e-287 Length: 1524
Score: 320.00 Matches: 320
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 28.4% Indels: 0
DB: 3 Gaps: 0

US-10-643-795a-123 (1-1127) x US-09-030-607-109 (1-1524)

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QY 766 LeuArgGInGlyLeuSerGlyGlyGlySerLeuAlaSerGlyGlyProGlyProGly 785
DB 10 CTGCGCCAGGCGCTGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGAGC 69
QY 786 HisAlaSerLeuSerGlnArgLeuArgLeuTyrLeuAlaAspSerTrpAngInGlyAsp 805
DB 70 CATGCTCTACCTAGCCAGCGGCGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 129
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Exhibit A

Qy	806	LeuValAlaLeuThrCysPheLeuLeuGlyValGlyCysArgLeuThrProGlyLeuThr	825
Db	130	CTAGTGGCTCTCACTGCTCTCTCTGAGGCTGGGCTCGAGCTGACCCCGAGTTTGAC	189
Qy	826	HisLeuGlyArgThrValLeuCysIleAspPheMetValPheThrValArgLeuLeuHis	845
Db	190	CACCTGGGCGGCACTGCTCTGAGATGACATTCAAGTTTTCAGGGTCCGGCTGTTTAC	249
Qy	846	IlePheThrValAsnIleGlnLeuGlyProIleValIleValSerIleMetMetLeys	865
Db	250	ATCTTCACGGTCACAAACAGCTGGGGCCCAAGATCTCATCTGTGACGAAGATGATGAAG	309
Qy	866	AspValPhePhePheLeuPhePheLeuGlyValTyrLeuValAlaTyrGlyValAlaThr	885
Db	310	GACGGTCTTCTTCTCTCTCTCTCTGAGCGTGTGGTGTGAGCTTAAGGGGTGGCCAGC	369
Qy	886	GluGlyLeuLeuArgProArgAspSerAspPheProSerIleLeuArgValPheTyr	905
Db	370	GAGGGGCTCTCGAGGCCACGGGACAGTACCTTCCCAATCTTGGCCGGCTCTTCTAC	429
Qy	906	ArgProTyrLeuGlnIlePheGlyGlnIleProGlnIleAspMetAspValAlaLeuMet	925
Db	430	CGTCCCTACCTGCAGATCTTGGGAGATTCCCCAGAGACATGAGCGTGGCCCTCATG	489
Qy	926	GluHisSerArgCysSerSerGluProGlyPheTyrPalAsiProProGlyValAlaIle	945
Db	490	GAGGACACCAACTGCTCTGCGAGGCCGGGCTTCTGGGACACCCCTCCGGGGCCCAAGCG	549
Qy	946	GlyThrCysValSerGlnTyrAlaAsnTyrLeuValIleLeuLeuValIlePheLeu	965
Db	550	GGCACCTGGTCTCCAGTATGCCAAGCTGGCTGGTGGTGGTCTCTGTCATCTTCTTG	609
Qy	966	LeuValAlaAsnIleLeuLeuValAsnLeuLeuIleAlaMetPheSerTyrThrPheGly	985
Db	610	CTCGGGGCCAATCTCTGCTGATCAACTGTCATTTGCCATGTTCAATTACATTCAGC	669
Qy	986	LysValGlnGlyAsnSerAspLeuTyrTyrIleValGlnIleArgTyrArgLeuIleArgGlu	1005
Db	670	AAAGTACAGGGGCACAGCGATCTTCACTGGAAGGCGAGCGCTTACCGCTCATCCGGGAA	729
Qy	1006	PheHisSerArgProAlaLeuAlaProProPheIleValIleSerHisLeuArgLeuLeu	1025
Db	730	TTCCACTCTGGCCCGCTGGCCCGCCCTTATGTCATCTCCACTGGGCTCTCTG	789
Qy	1026	LeuArgGlnLeuCysArgArgProArgSerProGlnProSerSerProAlaLeuGlnHis	1045
Db	790	CTCAGGCAATTGTGACAGCGACCCCGGAGCCCCCAGCCGCTCTCCCGGCTCGACAGAT	849
Qy	1046	PheArgValTyrLeuSerIleGlnIleGluArgIleLeuLeuThrTyrGlnSerValHis	1065
Db	850	TTCCGGGTTTACTTTCTTACGAAGCGCGAGAGCTGTCACTGAGGAATCCGCTGCAT	909
Qy	1066	LysGluAsnPheLeuLeuAlaArgAlaArgAspIleArgGlnSerAspSerGlnArgLeu	1085
Db	910	AAGGAGAACTTCTCTGTCGACGCCCTGAGCAAGCGGAGAGAGCATCTCGAGGCTGTG	969

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/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C9
/ CURRENT APPLICATION NUMBER: US/09/439,313
/ CURRENT FILING DATE: 1999-11-12
/ NUMBER OF SEQ ID NOS: 575
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 109
/ LENGTH: 1524
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-439-313-109

Alignment Scores:
Pred. No.:      8,44e-287      Length:      1524
Score:          320.00         Matches:      320
Percent Similarity: 100.0%     Conservative: 0
Best Local Similarity: 100.0%  Mismatches:    0
Query Match:     28.4%        Indels:       0
DB:              3            Gaps:         0

US-10-643-795A-123 (1-1127) x US-09-439-313-109 (1-1524)
QY      766 LeuArgGInGlyLeuSerGlyGlyGlySerLeuAlaSerGlyGlyProGlyProGly      785
DB      10 CTGCGCCAGGCGCTGAGGCGAGGCGGGGGGAGCCTCGCAGCGGGGGGCCCGGCGCTGCG      69
QY      786 HisAlaSerLeuSerGlnArgLeuArgLeuTyLeuAlaAspSerTrpAsnGlnCysAsp      805
DB      70 CATGGCTCAGTACGAGCAGCGCGCTGCGCTTCACTTCGCGGACAGCTGGAAACAGATGCGAC      129
QY      806 LeuValAlaIleuThrCysPheLeuLeuGlyValGlyCysArgLeuThrProGlyLeuTy      825
DB      130 CTAGGAGCTTCACCTGCTCTCTCTCTGAGCGGGCGGCGCTGACCCCGGGGTTGTAC      189
QY      826 HisLeuGlyArgThrValLeuCysIleAspPheMetValPheThrValArgLeuLeuHis      845
DB      190 CACCTGGGCGCGCATCTCTCTCTGCACTGCACTTCACTTCACGCGTTCACGCGTGCCTTAC      249
QY      846 IlePheThrValAsnIleGlnLeuGlyProIleValIleValSerIleMetCysIle      865
DB      250 ATCTTCACGGTCAACAAACAGCTGGGGCCAAAGATCGTATCGTAGCAAGATGATGAAG      309
QY      866 AspValPhePhePheLeuPhePheLeuGlyValTrpLeuValAlaTrpGlyValAlaThr      885
DB      310 GACGGTCTCTCTTCTCTCTCTCTCTCTGCGCGTGGCTGGTGAAGCCATGCGCGTGGCACG      369
QY      886 GlnGlyLeuLeuArgProArgAspSerAspPheProSerIleLeuArgArgValPheTy      905
DB      370 GAGGGGCTCTCGAGGCGACGGGACAGTGACTTCCCAAGTATCTGCGCGCGCTCTTAC      429
QY      906 ArgProTyLeuGlnIlePheGlyGlnIleProGlnIleAspMetAspValAlaLeuMet      925
DB      430 CGTCCCTACCTGCAATCTTGGGGGAGATTCCCGAGGAGCATGGAATGAGCGCTCATG      489
QY      926 GlnHisSerAsnCysSerSerSerGlnProGlyPheTrpAlaHisProProGlyValGlnAla      945
DB      490 GAGCACACACACTGCTCGTCGAGCGCGCGCTTCTGGGACACACCTTCGAGGCGCCAGGGG      549
QY      946 GlyThrCysValSerGlnTrpAlaAsnTrpLeuValValLeuLeuValIlePheLeu      965
DB      550 GGCACCTGGGTCTCCAGTATGCCAACTGGGCTGGTGTGCTCTCTCGTATCTTCCG      609
QY      966 LeuValAlaAsnIleLeuLeuValAsnLeuLeuIleAlaMetPheSerTyThrPheGly      985
DB      610 CTCGGGGCCAACTCTGCTGGTCAACTTGGCTCATTTGCATGTTCAAGTTACACATTCGGC      669
QY      986 LysValGlnGlyAsnSerAspLeuTyTrpIlyValGlnArgTyArgLeuIleArgGln      1000
DB      670 AAAGTACAGGGGCAACAGCATCTTACATCGAAGGGCGAGCGTTACCGCTCATCCGGGAA      729
QY      1006 PheHisSerArgProAlaLeuAlaProPheIleValIleSerHisLeuArgLeuLeu      1025
DB      730 TTCACCTCTCGGCGCGCGCTGCGCCCGCTTATCGTATCTCCACATTCGCGCTTCG      789

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06-APR-2001; 2001US-0281932P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0285859P.
XX
XX (E0SB-) EOS BIOTECHNOLOGY INC.
XX
XX
PI Glash KC, Mack DH, Wilson KE, Afar D, Hevezi P;
DR WPI; 2002-471335/50.
DR P-PSDB; ABG61852.
XX
XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
prostate tissue.
XX
XX
PS Claim 22; Page 339-340; 436pp; English.
XX
XX
CC The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 3810 BP, 669 A, 1177 C, 1203 G, 761 T, 0 U, 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 0 Length: 3810
XX Score: 1123.00 Matches: 1123
XX Percent Similarity: 100.0% Conservative: 0
XX Best Local Similarity: 100.0% Mismatches: 0
XX Query Match: 99.6% Indels: 0
XX DB: Gaps: 0
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US-10-643-795A-123 (1-1127) x ABK92167 (1-3810)
QY 5 ThThGulnYpProThraApMaLaTyRgYlGnLdeuAspPhThRgYlAaGlyARgYsHs 24
DB 3 ACCGAGAAAGCCACCGATGCTTACCGAGAGCTGAGCTTACCGGGGGCGCGCAAGCAC 62
QY 25 SerAanPheLeuArIgleuSerAaPArqThrAspProAlaAlaValIyrsrLeuValThr 44
DB 63 AGCAATTTCTCTCGGGCTCTCGAACCGAACGGAATCAAGCTGCAATTATATCTGTGCACA 122
QY 45 ArgThrTrpGlyPheArgAlaProAsnLeuValSerValLeuGlyGlySerGly 64
DB 123 CGCAACATGGGGCTTCGTGCCCCGACACTGTGTGTAAGTCTGGGGGAGATCGGGGGC 182
QY 65 ProValLeuGlnThrTrpLeuGlnAspLeuArqRgYlYeuValAArgAlaAlaGln 84
DB 183 CCGCTCTCCAGACCTGGCTGAGAGACTGTGTGTGTGTGGGGCTGTGGCGGGCTCCAG 242
QY 85 SerThrGlyAlaTrpIleValThrGlyGlyLeuHisThRgYlIleGlyARgHsValGly 104
DB 243 AGCACAGAGAGCTGATTTGTCTACCTGGGGGCTTGCACACGGGCACTGGCGGCAATGTGGT 302
QY 105 ValAlaValAArgAPhIsglMetAlSerThrGlyGlyThrIyValAlaIlaMetGly 124
DB 303 GTGGCTGTACGGGACCATCAGATGGCCAGACACTGGGGGCAACAAAGGTGTGGCATGGGT 362
QY 125 ValAlaProTrpGlyValAlaArgAanArqPThrIleuIleAanProIyGlySerPhe 144

Db	363	GTGGCCCCCTGGGGTGTGGTCGGAAATTAGACACCTCATCAACCCAGAGGCTCGTTCC	422
Qy	145	ProAlaArgTyraGTrpArgGlyAspProGluAspGlyValGlnPheProLeuAspTyr	164
Db	423	CTTCGAGAGGATACCGGTGGCGCGGTGACCCGGAGAGACGGGGTCCAGTTTCCCTTGACCTAC	482
Qy	165	AsnTyrSerAlaPhePheLeuValAspAspGlyTyrHisGlyCysLeuGlyGlyIleuAsn	184
Db	483	AACTACTCGGCTTCTTCTCTGTGTGACGACGGCACACACGGCTGCTGGGGGGCGAGAAC	542
Qy	185	ArgPheArgLeuArgLeuGlyIleuSerTyrTlleSerGlnGlnIleThrGlyValGlyGlyTyr	204
Db	543	CGCTTCGCGCTTGGCCCTGGAGTCTTACATCTCACACGACAAAGACGGGGCTGGAGGAGCT	602
Qy	205	GlyTlleAspIleProValLeuLeuLeuLeuIleAspGlyAspGlyIleuThrArg	224
Db	603	GGAAATTGACATCTCTGTCTCTGCTCTCTCTGATGATGATGATGAGAAAGATTGACGCGCA	662
Qy	225	IleGluAsnAlaThrGlnAlaGlnLeuProCysLeuLeuValAlaGlySerGlyGlyAla	244
Db	663	ATTAGGAACGCCCAACCGGCTCAGCTCCCATGTCTCTCTGTGGTGTGCTCAGGGAGCT	722
Qy	245	AlaAspCysLeuAlaGlyIleuThrLeuGluAspThrLeuAlaProGlySerGlyGlyAlaArg	264
Db	723	GCGGACTCCTCGGCGGAGACCTCGAAGACACTCTGGCCCCAGGAGATGGGGAGCCAGG	782
Qy	265	GlnGlyValAlaArgAspArgIleArgArgPhePheProIleuGlyAspLeuGluValLeu	284
Db	783	CAGGGCGAAGCCCGAGATCGAATACAGGCTTCTTCTTCCAAAGGGACCTTGAAGTCTCG	842
Qy	285	GlnAlaGlnValGluArgIleMetThrArgGlyGluLeuIleuThrValTyrSerSerGlu	304
Db	843	CAGGCCACGCTGGAGAGGATTAATGACCCGGAAAGAGCTCTCGACAGCTCTATTCTTCTGAG	902
Qy	305	AspGlySerGlnGluPheGlnThrTlleValLeuValAlaLeuValIleValCysGlySer	324
Db	903	GATGGGTCTGAGGAATTCGAGACCACTAATTGTGAAGGCCCTTGTGAAGCCTGTGGAGC	962
Qy	325	SerGlnAlaSerAlaTyrLeuAspGlyLeuArgLeuAlaValAlaIlePheAsnArgValAsp	344
Db	963	TGGAGGCTCAGCTTACCTGATGATGAGTGGCTTGGCTGTGGTGGAAACGGGTGGAC	1022
Qy	345	IleAlaGlnSerGluLeuPheArgGlyAspIleGlnTrpArgSerPheHisLeuGluAla	364
Db	1023	ATTGCCAAGTGAACCTCTTTCGGGGGAGATCCCAATGGCGGTCTTCCATCTCGAAGCT	1082
Qy	365	SerLeuMetAspAlaLeuLeuAsnAspArgProGluPheValArgLeuLeuIleSerHis	384
Db	1083	TTCCTCATGACGCGCTGCTGAAATACCGGCTGTGGTTCGTGGCTTCTCATTTCCAC	1142
Qy	385	GlyLeuSerLeuGlyHisPheLeuThrProMetArgLeuAlaGlnLeuTyrSerAlaIle	404
Db	1143	GGCTTAGGCTGGGCGACTTCTTGACCCCGATGCCCTGGCCCACTTACAGCGCGGGG	1202
Qy	405	ProSerAsnSerLeuIleArgAsnLeuLeuAspGlnAlaSerHisSerAlaGlyTyrIle	424
Db	1203	CCCTTCAATCTCGTCACTCCGCAACTTTTGGACACAGGCTCCCAACAGCGCAGACACAA	1262
Qy	425	AlaProAlaLeuArgGlyGlyAlaAlaGluLeuArgProPheAspValGlyHisValLeu	444
Db	1263	GCCCAAGCCCTTAAAGGAGAGCTGGGAGCTCGGCCCCCTGACGTGGGGCATGTGGCTG	1322
Qy	445	ArgMetLeuLeuGlyIleuMetCysAlaProArgTyrProSerGlyGlyValaIlePhePro	464
Db	1323	AGGATGTGCTGGGGAGAAAGTGGCGGCGAGGATCACTTCCGGGGGCGCCTGGGACCT	1382
Qy	465	HisProGlyGlnGlyPheGlyGlyIleuSerMetTyrLeuLeuSerAspValaIleThrSerPro	484
Db	1383	CACCCAGGCGAGGGCTTCCGGGAGAGCAGTATGTGCTCTCGGACAAAGCCACCTCGCGG	1442
Qy	485	LeuSerLeuAspAlaGlyLeuGlyGlnAlaProTyrPheAspLeuLeuThrAlaLeu	504

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